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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Mon Aug 13 16:26:09 EDT 2007

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Application No: 10716293 Version No: 2.1

**Input Set:**

**Output Set:**

**Started:** 2007-08-13 16:25:30.258  
**Finished:** 2007-08-13 16:25:33.289  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 31 ms  
**Total Warnings:** 218  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 218  
**Actual SeqID Count:** 218

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
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W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

**Input Set:**

**Output Set:**

**Started:** 2007-08-13 16:25:30.258  
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Error code      Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> MASSIA, STEPHEN P.  
EHTESHAMI, GHOLAM R.

<120> THERAPEUTIC BIOCONJUGATES

<130> AZTE:015US

<140> 10716293  
<141> 2003-11-17

<150> 10/295,734  
<151> 2002-11-15

<160> 218

<170> PatentIn version 3.2

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1 5 10 15  
  
caa tat 54  
Gln Tyr

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<212> PRT  
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<220>  
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Gln Tyr

<210> 3  
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<220>  
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<220>  
<221> CDS  
<222> (1)..(15)

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Gln Thr Ser Gln Tyr  
1 5

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<211> 5  
<212> PRT  
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Gln Thr Ser Gln Tyr  
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<210> 5  
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<220>  
<221> CDS  
<222> (1)..(15)

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ata gca gta ata gga 15  
Ile Ala Val Ile Gly  
1 5

<210> 6

<211> 5  
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Ile Ala Val Ile Gly  
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<210> 7  
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Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys  
1 5 10 15

acc cag gtc ggt ctg ata caa tat gcg aat aat cca cgc tgg ttc aat 96  
Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Trp Phe Asn  
20 25 30

cta aat act tat aag act aag gaa gag atg att gtt gct acc tcc cag 144  
Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln  
35 40 45

act agc cag tac ggc ggt gat cta aca aat aca ttc gga gcg atc cag 192  
Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile Gln  
50 55 60

tat gcg cga aaa tat gcg tat tca gcg gcc tct gga ggc cgt cga agt 240  
Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg Ser  
65 70 75 80

gca aca ctt aaa gta atg gtg 261  
Ala Thr Leu Lys Val Met Val  
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1 5 10 15

Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Trp Phe Asn  
20 25 30

Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln  
35 40 45

Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile Gln  
50 55 60

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65 70 75 80

Ala Thr Leu Lys Val Met Val  
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<210> 9

<211> 294

<212> DNA

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<220>

<221> CDS

<222> (1)..(294)

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Tyr Asn Val Asp Thr Glu Ser Ala Leu Leu Tyr Gln Gly Pro His Asn  
1 5 10 15

aca ctg ttt ggc tac agt tgg ctc cac tcc cat gga gct cat aga tgg 96  
Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp  
20 25 30

cta ctg gta gga gcg cca aca gca atg tgg tta gca atg gca agc gtt 144  
Leu Leu Val Gly Ala Pro Thr Ala Met Trp Leu Ala Met Ala Ser Val  
35 40 45

att aat cct ggg gcc atc tat aga tgc aga ata gga aaa aac cca ggg 192  
Ile Asn Pro Gly Ala Ile Tyr Arg Cys Arg Ile Gly Lys Asn Pro Gly

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cag acg tgt gaa ttg caa ttg ggt tca ttc cac ggt gag ccc ggc ggt			240
Gln Thr Cys Glu Leu Gln Leu Gly Ser Phe His Gly Glu Pro Gly Gly			
65	70	75	80
aag act tgt cta gag gaa aga gat cac caa tgg ctt ggg gtg acc ctc			288
Lys Thr Cys Leu Glu Glu Arg Asp His Gln Trp Leu Gly Val Thr Leu			
85	90	95	
tcg aga			294
Ser Arg			

<210> 10			
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1	5	10	15
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20	25	30	
Leu Leu Val Gly Ala Pro Thr Ala Met Trp Leu Ala Met Ala Ser Val			
35	40	45	
Ile Asn Pro Gly Ala Ile Tyr Arg Cys Arg Ile Gly Lys Asn Pro Gly			
50	55	60	
Gln Thr Cys Glu Leu Gln Leu Gly Ser Phe His Gly Glu Pro Gly Gly			
65	70	75	80
Lys Thr Cys Leu Glu Glu Arg Asp His Gln Trp Leu Gly Val Thr Leu			
85	90	95	
Ser Arg			

<210> 11			
<211> 156			
<212> DNA			
<213> Artificial Sequence			

<220>  
<223> Description of Artificial Sequence: Integrin

<220>  
<221> CDS  
<222> (1)..(156)

<400> 11  
cag gat tat gta aag aaa ttc ggc gaa cat ttt gca agt tgt caa gca 48  
Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala  
1 5 10 15

ggg ata tcc tcg ttc tat acg aaa gac tta atc gta atg ggt gca cca 96  
Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro  
20 25 30

gga tct tca tac tgg aca gga agc tta ttt gta tac atg att acc act 144  
Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr  
35 40 45

aat aag tat aaa 156  
Asn Lys Tyr Lys  
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<210> 12  
<211> 52  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: Integrin

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Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala 156  
1 5 10 15

Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro  
20 25 30

Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr  
35 40 45

Asn Lys Tyr Lys  
50

<210> 13  
<211> 156  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Integrin

<220>  
<221> CDS  
<222> (1)..(156)

<400> 13  
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Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala  
1 5 10 15

ggg ata tcc tcg ttc tat acg aaa gac tta atc gta atg ggt gca cca 96  
Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro  
20 25 30

gga tct tca tac tgg aca gga agc tta ttt gta tac atg att acc act 144  
Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr  
35 40 45

aat aag tat aaa 156  
Asn Lys Tyr Lys  
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<210> 14  
<211> 52  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: Integrin

<400> 14  
Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala  
1 5 10 15

Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro  
20 25 30

Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr  
35 40 45

Asn Lys Tyr Lys  
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<210> 15  
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<212> DNA  
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Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys Asn Glu Asn Lys Leu  
1 5 10 15

cca aca gga gga 60  
Pro Thr Gly Gly  
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1 5 10 15

Pro Thr Gly Gly  
20

<210> 17  
<211> 33  
<212> DNA  
<213> Artificial Sequence

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<220>  
<221> CDS  
<222> (1)..(33)

<400> 17 33  
gga gga gca cca cag cat gaa caa ata gga aaa  
Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys  
1 5 10

<210> 18

<211> 11  
<212> PRT  
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<400> 18

Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys  
1 5 10

<210> 19  
<211> 18  
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<223> Description of Artificial Sequence: Integrin

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<221> CDS  
<222> (1)..(18)

<400> 19  
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Ser Tyr Trp Thr Gly Ser  
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<210> 20  
<211> 6  
<212> PRT  
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<400> 20

Ser Tyr Trp Thr Gly Ser  
1 5

<210> 21  
<211> 33  
<212> DNA  
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<221> CDS

<222> (1)..(33)

<400> 21

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Met Gly Ala Pro Gly Ser Ser Tyr Trp Thr Gly  
1 5 10

33

<210> 22

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Integrin

<400> 22

Met Gly Ala Pro Gly Ser Ser Tyr Trp Thr Gly  
1 5 10

<210> 23

<211> 111

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Integrin

<220>

<221> CDS

<222> (1)..(111)

<400> 23

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Tyr Asn Val Asp Thr Glu Ser Ala Leu Leu Tyr Gln Gly Pro His Asn  
1 5 10 15

48

aca ttg ttt ggg tat agt tgg ctt cat agt cat gga gca cac aga tgg  
Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp  
20 25 30

96

ctg cta gta ggc gca

111

Leu Leu Val Gly Ala

35

<210> 24

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Integrin

<400> 24

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1 5 10 15

Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp  
20 25 30

Leu Leu Val Gly Ala  
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<210> 25

<211> 225

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Integrin

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<221> CDS

<222> (1)..(225)

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Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys His  
1 5 10 15

gaa aac aaa tta cca aca gga ggg tgt tat ggc gtg ccc ccg gat tta 96  
Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro Asp Leu  
20 25 30

aga acc gaa tta agt aag aga ata gcc cct ggt tat cag gac tac gtt 144  
Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Gly Tyr Gln Asp Tyr Val  
35 40 45

aaa aag ttc gga gag cat ttt gct agt tgc caa gca ggt atc agt agt 192  
Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala Gly Ile Ser Ser  
50 55 60

ttc tac act aag gat tta att gtc atg ggg gcg 225  
Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala  
65 70 75

<210> 26

<211> 75

<212> PRT

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<400> 26

Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys His  
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Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro Asp Leu  
20 25 30

Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Gly Tyr Gln Asp Tyr Val  
35 40 45

Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala Gly Ile Ser Ser  
50 55 60

Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala  
65 70 75

<210> 27

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<222> (1)..(222)

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Tyr Met Ile Thr Thr Asn Lys Tyr Lys Ala Phe Leu Gly Lys Gln Asn  
1 5 10 15

cag gtg aag cca gga agt tat tta ggg tat agt gta ggt gcc ggc cat 96  
Gln Val Lys Pro Gly Ser Tyr Leu Gly Tyr Ser Val Gly Ala Gly His  
20 25 30

ttc aga ag